

neighboring the junction between the first and second sequence. If the sequence elements are exons, the joining sequence is the 3' sequence of one exon and 5' sequence of another exon. The joining sequence should be at least 20 bases in length, preferably at least 30 bases in length, more preferably at least 40 bases in length, even more preferably at least 50 bases and most preferably 100 bases in length.

#### IN THE CLAIMS

Kindly enter the following amendments to claim 1:

1. (amended) A nucleic acid probe array comprising a set of probes to interrogate the joining sequence between a first sequence element and a second sequence element.

#### REMARKS

Applicant would like to thank the Examiner for the courtesy extended during an interview with Applicant's representative, Mr. W. Zhou and providing a complimentary fax copy of the Office Action.

Applicant has amended claim 1 for the purpose of expediting the issuance of claims. Support for the amendment to claim 1 is found throughout the application and is particularly found on page 4, lines 3-13. It is respectfully submitted that no new matter has been introduced by the present amendments and entry of the same is respectfully requested.

By these amendments, the Applicant does not acquiesce to the propriety of any of the Examiner's rejections and do not disclaim any subject matter to which Applicant is entitled.

#### ***Rejection Under 35 U.S.C. § 102(b)***

The Examiner has rejected claims 1-3, 5, 6 as rejected under 35 U.S.C. 102(b) as being anticipated by Cronin *et. al.* (WO 98/30883, published July 16, 1998). Applicant respectfully traverses this rejection.

Cronin teaches that its invention provides arrays of probes immobilized on a solid support for analyzing biotransformation genes. In contrast, Applicant recites joining